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(TM)

MSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat May 13 09:29:15 2000; Maspar time 3.98 seconds
Tabular output not generated. 267.936 Million cell updates/sec

Title: >US-09-331-631-1
Description: (29-73) from US09331631.pep (2 of 5)
Perfect score: 361
Sequence: 1 SEFDROEYECRCQCMQLETSQGMRCVSCQDKRFEEDIMSKYD 45

Scoring table:
PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseg35
1:genesegp

Statistics: Mean 24.753; Variance 88.190; scale 0.281

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	361	100.0	666	1 W62829	Macadamia integrifolia	2.58e-30
2	361	100.0	666	1 W62828	Macadamia integrifolia	2.58e-30
3	259	71.7	625	1 W62830	Macadamia integrifolia	9.96e-19
4	109	30.2	590	1 W62832	Gossypium hirsutum ant	1.26e-02
5	97	26.9	525	1 W62831	Theobroma cacao antim	1.88e-01
6	97	26.9	566	1 R20181	Sequence encoded by 67	1.88e-01
7	95	26.3	218	1 W40287	Human TSP1 protein.	2.93e-01
8	95	26.3	239	1 R40823	Human thrombospondin 1	2.93e-01
9	95	26.3	441	1 W40288	Human concanamerised T	1.38e-01
10	77	21.3	62	1 W03698	Maize id gene product.	1.38e-01
11	77	21.3	409	1 W90342	G. max truncated SBP2	1.39e+01
12	77	21.3	438	1 W59836	Maize id protein.	1.39e+01
13	77	21.3	444	1 W90340	G. max truncated SBP1	1.39e+01
14	77	21.3	489	1 W90341	G. max truncated SBP1	1.39e+01
15	77	21.3	524	1 W90339	G. max SBP1 protein.	1.39e+01
16	73	20.2	81	1 Y12435	Human 5' EST secreted	3.18e+01
17	73	20.2	125	1 R13329	HE4 epididymis-specific	3.18e+01
18	73	20.2	124	1 W81779	Human HE4 protein.	3.18e+01
19	73	20.2	1284	1 P81187	Sequence encoded by a	3.18e+01
20	72	19.9	593	1 W62835	Zea mays antimicrobial	3.90e+01
21	72	19.9	1416	1 R67358	Human astrovirus serot	3.90e+01
22	71	19.7	2703	1 R70236	P. falciparum Pfoj3.	4.77e+01
23	71	19.7	2710	1 W22482	Plasmodium Pfoj3.	4.77e+01

24	71	19.7	3060	1 W22475	Plasmodium var-7.	4.77e+01
25	70	19.4	103	1 Y11721	Human 5' EST secreted	5.83e+01
26	70	19.4	191311	1 R91311	N. gonorrhoeae glycosyl	5.83e+01
27	70	19.4	348	1 W06576	Neisseria polyglycosyl	5.83e+01
28	69	19.1	348	1 W62836	Zea mays antimicrobial	7.13e+01
29	69	19.1	35	1 R21079	Antimicrobial maize pe	7.13e+01
30	68	18.8	623	1 W30622	Arabidopsis enhanced p	8.70e+01
31	68	18.8	816	1 R85870	WD-40 domain-contg. Mu	8.70e+01
32	68	18.8	1479	1 W41119	Human type C lectin.	8.70e+01
33	67	18.6	203	1 Y04837	Mycobacterium species	1.06e+02
34	67	18.6	363	1 R47557	ILTV thymidine kinase.	1.06e+02
35	67	18.6	506	1 Y04841	Mycobacterium species	1.06e+02
36	67	18.6	974	1 W55960	Human transient recept	1.06e+02
37	66	18.3	30	1 W08904	(Cyclo 30-33)ID-Phe12,	1.29e+02
38	66	18.3	38	1 W07823	Cyclic corticotrophin	1.29e+02
39	66	18.3	194	1 R57061	P. aeruginosa muc.	1.29e+02
40	66	18.3	370	1 W54097	Homo sapiens B223 sequ	1.29e+02
41	66	18.3	676	1 R81473	Thermus aquaticus DNA	1.29e+02
42	66	18.3	676	1 W80302	A thermophilic ligase	1.29e+02
43	66	18.3	680	1 R15299	Thermotable T. aquati	1.29e+02
44	66	18.3	1496	1 Y04136	Human slit 3 mature pr	1.29e+02
45	66	18.3	1523	1 Y04137	Human slit 3 protein.	1.29e+02

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	W62829: standard; protein; 666 AA.	
AC	W62829: (first entry)	
DT	27-DEC-1998	
DE	Macadamia integrifolia antimicrobial protein.	
KW	antimicrobial protein; infestation; control.	
OS	Macadamia integrifolia.	
FH	Key	Location/Qualifiers
FT	Peptide	1..28
FT	Protein	/note= "signal peptide"
FT		29..666
FT		/note= "mature protein"
PN	W09827805-A1.	
PD	02-JUL-1998	
PR	22-DEC-1997; AU0874	
PA	(RTR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;	
DR	WPI: 98-377279/32.	
DR	N-PSDB: V42311	
PT	Novel anti-microbial protein from e.g. Macadamia integrifolia -	
PT	useful for controlling microbial infestations of plants or mammals	
PS	Claim 1; Page 39-41; 96pp; English.	
CC	The sequence is that of an antimicrobial protein which can	
CC	be used to control microbial infestations in plants and mammalian	
CC	animals.	
CC	Sequence 666 AA;	
SQ		
Db	29 SEFDROEYECRCQCMQLETSQGMRCVSCQDKRFEEDIMSKYD 73	
Oy	29 SEFDROEYECRCQCMQLETSQGMRCVSCQDKRFEEDIMSKYD 73	
RESULT	2	
ID	W62828: standard; protein; 666 AA.	
AC	W62828: (first entry)	
DT	27-OCT-1998	
DE	Macadamia integrifolia antimicrobial protein.	
KW	antimicrobial protein; infestation; control.	
OS	Macadamia integrifolia.	
FH	Key	Location/Qualifiers
FT	Peptide	1..28
FT		/note= "signal peptide"

FT Protein 29..666
/note="mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997: AU0874.
PR 20-DEC-1996: AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42310.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PS Claim 1; Page 34-36; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;
Query Match 100.0%; Score 361; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.58e-30;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 SEFPDREYEECKRCQMLETSGOMRCVSOCDKRFEDIDMSKYD 73
QY 29 SEFPDREYEECKRCQMLETSGOMRCVSOCDKRFEDIDMSKYD 73
RESULT 3
ID W62830 standard; Protein; 625 AA.
AC W62830:
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key location/Qualifiers
FT Peptide 1..28
/note="signal peptide"
FT Protein 29..666
/note="mature protein"
FN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997: AU0874.
PR 20-DEC-1996: AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42316.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PS Claim 1; Page 43-45; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 625 AA;
Query Match 71.7%; Score 259; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 9.96e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 QCMOLETSGOMRCVSOCDKRFEDIDMSKYD 32
QY 42 QCMOLETSGOMRCVSOCDKRFEDIDMSKYD 73
RESULT 4
ID W62832 standard; Protein; 590 AA.
AC W62832:
DT 27-OCT-1998 (first entry)
DE Gossypium hirsutum antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Gossypium hirsutum.
PN W09827805-A1.
PD 02-JUL-1998.

PF 22-DEC-1997: AU0874.
PR 20-DEC-1996: AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42310.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PS Claim 1; Page 49-51; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 590 AA;
Query Match 30.2%; Score 109; DB 1; Length 590;
Best Local Similarity 45.2%; Pred. No. 1.26e-02;
Matches 14; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
Db 87 YEEQCEKRCQOEER-QPQOCRCRKRFED 116
QY 36 YEECKRCQMLETSGOMRCVSOCDKRFED 66
RESULT 5
ID W62831 standard; Protein; 525 AA.
AC W62831:
DT 27-OCT-1998 (first entry)
DE Theobroma cacao antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Theobroma cacao.
PN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997: AU0874.
PR 20-DEC-1996: AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42316.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PS Claim 1; Page 47-49; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 525 AA;
Query Match 26.9%; Score 97; DB 1; Length 525;
Best Local Similarity 31.4%; Pred. No. 1.88e-01;
Matches 11; Conservative 11; Mismatches 12; Indels 1; Gaps 1;
Db 39 ROOYEQCRCESEATEBEQCEQRCEREYKEQ 73
QY 33 ROYEECKRCQMLETSGOMR-RCVSOCDKRFED 66
RESULT 6
ID R20181 standard; Protein; 566 AA.
AC R20181:
DT 16-APR-1992 (first entry)
DE Sequence encoded by 67 kD T. cacao protein cDNA.
KW Cocoa; flavour; vicillin; seed storage protein.
OS Theobroma cacao.
PN W09119801-A.
PD 26-DEC-1991.
PE 07-JUN-1991: G00914.
PR 11-JUN-1990: GB-013016.
PA (MRSC) MARS UK LTD.
PI Spencer ME, Hodge R, Deakin EA, Ashton S;
DR WPI: 92-024418/03.
DR N-PSDB: Q20377.
PT Recombinant cocoa proteins - are responsible for flavour in cocoa
PT beans and produced in large quantities using yeast and bacterial
PT expression vectors
PS Claim 4; Fig 2; 59pp; English.
CC The inventors claim a 67 kD and 31 kD T. cacao protein, and

Db 116 SSVQTRTCHIOECRKRFKDGWS 139
 :| | | :| | | | | :| |
 Oy 48 TSGMRRC-VSQCKRFEEDIDW 70

RESULT 10
 ID W03698 standard; Protein: 62 AA.

AC W03698;
 DT 06-MAR-1997 (first entry)
 DE Maize Id gene product.
 KW Maize: Zea mays; Id: id*; transposon; transposable element;
 KM Ds2; flower evocation; zinc-finger regulatory protein.

OS Zea mays.
 PN W09634088-A2.
 PD 31-OCT-1996.
 PF 15-MAR-1996; U03466.
 PZ 15-MAR-1995; US-406186.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Colasanti JJ, Sundaresan V;
 DR WPI: 96-497621/49.
 DR N-PSDB: T42174, T42175.

PZ New isolated plant id gene - used to develop prods. for use in
 PT altering the induction of flowering in plants
 PS Claim 7, Fig 3 and Fig 5, 58pp; English.
 CC The id gene controls flower evocation in maize plants. The
 CC maize nucleic acid is similar to that of genes encoding zinc-
 CC finger regulatory proteins in animals.
 CC Transposons Ac and Ds constitute a family of related transposable
 CC elements present in maize. A derivative of Ds, Ds2, can be used
 CC to produce a new mutant of the id gene. The Ds2 (in the presence
 CC of active Ac) is excised from a nearby gene on chromosome 1
 CC and inserted into the id gene to produce id*.
 SO Sequence 62 AA;

Query Match 21.3%; Score 77; DB 1; Length 62;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 17 GKRWCRCRGKPYAVQSDW 36
 :| | | | :| | :| |
 Oy 50 GMRRCVSGCKRFEEDIDW 69

RESULT 11
 ID W90342 standard; Protein: 409 AA.

AC W90342;
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP2 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 OS Glycine max.
 PN W09853086-A1.
 PD 26-NOV-1998.
 PE 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI: 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 PS Claim 7; Page 39-40; 58pp; English.
 CC This sequence represents a novel SBP2 protein. SBP2 is used in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content

CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 SO Sequence 409 AA;

Query Match 21.3%; Score 77; DB 1; Length 409;
 Best Local Similarity 45.8%; Pred. No. 1.39e+01;
 Matches 11; Conservative 6; Mismatches 5; Indels 2; Gaps 2;

Db 42 CKHCCGQKQRTESDKRFLQCCD 65
 :| | | | :| | | | :| |
 Oy 39 CKRCQMDL-E-TSGMRRCVSGCD 60

RESULT 12
 ID W59836 standard; Protein: 438 AA.

AC W59836;
 DT 16-NOV-1998 (first entry)
 DE Maize Id protein.
 KW Maize; Id: floral induction; transgenic plant.

OS Zea mays.
 PN W09837201-A1.
 PD 27-AUG-1998.
 PF 18-FEB-1998; U03161.
 PR 30-DEC-1997; US-000640.
 PA 20-FEB-1997; US-804104.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Colasanti JJ, Sundaresan V;
 DR WPI: 98-467364/40.
 DR N-PSDB: V41721.

PT Id gene controlling floral induction in maize - useful to create
 PT transgenic plants with earlier, delayed or inhibited floral
 PT induction e.g. to extend geographical range of crops
 PS Claim 5, Fig 3, 68pp; English.
 CC The maize id gene controls floral induction and is useful in the
 CC production of transgenic plants with altered floral induction times,
 CC i.e. earlier, delayed or inhibited floral induction. The id gene and
 CC zinc-finger regulatory regions are useful to identify these genes in
 CC maize and isolate similar genes in other plants. The polypeptides
 CC and antibodies are also useful in id detection e.g. to locate activity in
 CC plants.
 SO Sequence 438 AA;

Query Match 21.3%; Score 77; DB 1; Length 438;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 187 GKRWCRCRGKPYAVQSDW 206
 :| | | | :| | | | :| |
 Oy 50 GMRRCVSGCKRFEEDIDW 69

RESULT 13
 ID W90340 standard; Protein: 444 AA.

AC W90340;
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP1 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 OS Glycine max.
 PN W09853086-A1.
 PD 26-NOV-1998.
 PE 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI: 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds

PS Claim 7: Page 36-37; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 444 AA;

Query Match 21.3%; Score 77; DB 1; Length 444;
Best Local Similarity 44.4%; Pred. No. 1.39e+01;
Matches 12; Conservative 6; Mismatches 6; Indels 3; Gaps 2;

DB 43 CKHCCOQOQYEGDKRVCQSCD-RY 68
QY 39 CKRCCMOLE--TSGQMRVCVSCDKRF 63

RESULT 14
ID W90341 standard; protein: 489 AA.
AC W90341;
DT 24-MAY-1999 (first entry)
DE G. max SBP2 protein.
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN MO9853086-A1.
PD 26-NOV-1998.
PE 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNITV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI: 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 13b: Page 37-38; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 489 AA;

Query Match 21.3%; Score 77; DB 1; Length 489;
Best Local Similarity 45.8%; Pred. No. 1.39e+01;
Matches 11; Conservative 6; Mismatches 5; Indels 2; Gaps 2;

DB 42 CKHCCOQOQYEGDKRVCQSCD 65
QY 39 CKRCCMOLE--TSGQMRVCVSCDKRF 60

RESULT 15
ID W90339 standard; protein: 524 AA.
AC W90339;
DT 24-MAY-1999 (first entry)
DE G. max SBP1 protein.

KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN MO9853086-A1.
PD 26-NOV-1998.
PE 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNITV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI: 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Disclosure: Page 34-36; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 524 AA;

Query Match 21.3%; Score 77; DB 1; Length 524;
Best Local Similarity 44.4%; Pred. No. 1.39e+01;
Matches 12; Conservative 6; Mismatches 6; Indels 3; Gaps 2;

DB 43 CKHCCOQOQYEGDKRVCQSCD-RY 68
QY 39 CKRCCMOLE--TSGQMRVCVSCDKRF 63

Search completed: Sat May 13 09:29:23 2000
Job time : 8 secs.

